



SEQUENCE LISTING

<110> Lead B.V.
NOTEBORN, Mathieu Hubertus Maria
DAMEN-VAN OORSCHOT, Astrid Adriana Anna Maria

<120> MOLECULES INTERACTING WITH APOPTIN

<130> 2906-5008

<140> 09/551981

<141> 2000-06-26

<150> PCT/NL98/00687

<151> 1998-12-03

<150> EP 97203781.6

<151> 1997-12-12

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<223> pACT-specific sequencing primer

<400> 1

taccactaca atggatg

17

<210> 2

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<223> Hou/Nmi-like protein putative immunogenic peptide

<400> 2

Arg Asn Gly Gly Gly Glu Val Asp Arg Val Asp Tyr Asp Arg Gln
1 5 10 15

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> misc_feature

<223> IFP35-like protein putative immunogenic peptide

<400> 3

Cys Gln Leu Arg Lys Glu Leu Gly Asp Ser Pro Lys Asp Lys Val Pro
1 5 10 15

<210> 4

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(658)

<223> for any n in the sequence, n is an undefined base

<400> 4

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gggggatcat ggaagctgat aaagatgaca cacaacaaat tcttaaggag cattcgccag      60
atgaatttat aaaagatgaa caaataagg gactaattga tgaaattaca aagaaaaata      120
ttcaactaaa gaaggagatc caaaagcttg aaacggaggtt acaagaggct accaaagaat      180
tccagattaa agaggatatt cctgaaacaa agatgaaatt cttatcagtt gaaactcctg      240
agaatgacag ccagttgtca aatatctcct gttcgtttca agtgagctcg aaagttcctt      300
atgagataca aaaaggacaa gcacttatca cctttgaaaa agaagaagtt gctcaaaatg      360
tggttaagcat gagtaaacad catgtacaga taaaagatgt aaatctggag gttacggcca      420
agccagttcc attaaattca ggagtcagat tccaggttta tgtagaagtt tctaaaatga      480
aaatcaatgt tactgaaatt cctgacacat tgcgtgaaga tcaaatgaga gacaaactag      540
agctgagctt ttcaaagtcc cgaaatggga ggcggagang tggaccgcgt gggactatga      600
cagacagtcc gggagtgcag tcatcacgtt tggnggagat tgggagtggc tgacannn      658
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<210> 5

<211> 719

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(719)

<223> for any n in the sequence, n is an undefined base

<400> 5

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cggagttaca agaggctacc aaagaattcc agattaaaga ggatattcct gaaacaaaga      60
tgaaattctt atcagttgaa actcctgana atgacagcca gttgtcaa atctcctggt      120
cgtttcaagg tgagctcgaa agttccttat gagatacaaa aaggacaatg cacttatcac      180
ctttgaaaaa ggaagaagtt gctcaaaatg tgnngtaangc atgagtaa atcatgtaca      240
gataataaga tgtaaactctg gaggttacgg ccaaagccaa gttccattaa tattcaagga      300
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gtcangattc cagngtttat gctagaangt ttctaaaaat ganaatcaat ggttactgga 360
aattcctgga cacattgcgn tgaaagatca agatgacgaa gacaaactaa gaagctgagc 420
ttttcaaaag tcccgaana tggaagagcg gtagaggggtg gnaccgcgtg nganctatga 480
caagacaagn ccggggaagn tgcagtccat cacgtttgtn ngaagattgg angtnnggctg 540
accaangaat ttgaaaaag gagangaatt acccctcttt angagtaana tcaaaaccct 600
gccataanaa gttactgggt ttnccccatt acacagnant tacamnttga ncaanantan 660
ncaggataat ttncagggga anaatctnaa gnatggcaag ntgacttctg gacaanggt 719

<210> 6
<211> 220
<212> PRT
<213> Homo sapiens

<400> 6

His	Glu	Gly	Arg	Gly	Ile	Met	Glu	Ala	Asp	Lys	Asp	Asp	Thr	Gln	Gln	1	5	10	15
Ile	Leu	Lys	Glu	His	Ser	Pro	Asp	Glu	Phe	Ile	Lys	Asp	Glu	Gln	Asn	20	25	30	
Lys	Gly	Leu	Ile	Asp	Glu	Ile	Thr	Lys	Lys	Asn	Ile	Gln	Leu	Lys	Lys	35	40	45	
Glu	Ile	Gln	Lys	Leu	Glu	Thr	Glu	Leu	Gln	Glu	Ala	Thr	Lys	Glu	Phe	50	55	60	
Gln	Ile	Lys	Glu	Asp	Ile	Pro	Glu	Thr	Lys	Met	Lys	Phe	Leu	Ser	Val	65	70	75	80
Glu	Thr	Pro	Glu	Asn	Asp	Ser	Gln	Leu	Ser	Asp	Ile	Ser	Cys	Ser	Phe	85	90	95	
Gln	Val	Ser	Ser	Lys	Val	Pro	Thr	Glu	Ile	Gln	Lys	Gly	Gln	Ala	Leu	100	105	110	
Ile	Thr	Phe	Glu	Lys	Glu	Glu	Val	Ala	Gln	Asn	Val	Val	Ser	Met	Ser	115	120	125	
Lys	His	His	Val	Gln	Ile	Lys	Asp	Val	Asn	Leu	Glu	Val	Thr	Ala	Lys	130	135	140	
Pro	Val	Pro	Leu	Asn	Ser	Gly	Val	Arg	Phe	Gln	Val	Thr	Val	Glu	Val	145	150	155	160
Ser	Lys	Met	Lys	Ile	Asn	Val	Thr	Glu	Ile	Pro	Asp	Thr	Leu	Arg	Glu	165	170	175	
Asp	Gln	Met	Arg	Arg	Lys	Leu	Glu	Leu	Ser	Phe	Ser	Lys	Ser	Arg	Asn	180	185	190	

Gly Arg Arg Arg Cys Gly Pro Arg Gly Thr Met Thr Asp Ser Pro Gly
 195 200 205

Val Gln Ser Ser Arg Leu Val Glu Ile Gly Ser Gly
 210 215 220

<210> 7
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 7

Met Glu Ala Asp Lys Asp Asp Thr Gln Gln Ile Leu Lys Glu His Ser
 1 5 10 15

Pro Asp Glu Phe Ile Lys Asp Glu Gln Asn Lys Gly Leu Ile Asp Glu
 20 25 30

Ile Thr Lys Lys Asn Ile Gln Leu Lys Lys Glu Ile Gln Lys Leu Glu
 35 40 45

Thr Glu Leu Gln Glu Ala Thr Lys Glu Phe Gln Ile Lys Glu Asp Ile
 50 55 60

Pro Glu Thr Lys Met Lys Phe Leu Ser Val Glu Thr Pro Glu Asn Asp
 65 70 75 80

Ser Gln Leu Ser Asn Ile Ser Cys Ser Phe Gln Val Ser Ser Lys Val
 85 90 95

Pro Tyr Glu Ile Gln Lys Gly Gln Ala Leu Ile Thr Phe Glu Lys Glu
 100 105 110

Glu Val Ala Gln Asn Val Val Ser Met Ser Lys His His Val Gln Ile
 115 120 125

Lys Asp Val Asn Leu Glu Val Thr Ala Lys Pro Val Pro Leu Asn Ser
 130 135 140

Gly Val Arg Phe Gln Val Thr Val Glu Val Ser Lys Met Lys Ile Asn
 145 150 155 160

Val Thr Glu Ile Pro Asp Thr Leu Lys Glu Asp Gln Met Arg Asp Lys
 165 170 175

Leu Glu Leu Ser Phe Ser Lys Phe Arg Asn Gly Gly Gly Glu Val Asp
 180 185 190

Arg Val Asp Tyr Asp Arg Gln Ser Gly Ser Ala Val Ile Thr Phe Val
 195 200 205

Glu Ile Gly Val Ala Asp Lys Ile Leu Lys Lys Lys Glu Tyr Pro Leu
 210 215 220

Tyr Ile Asn Gln Thr Cys His Arg Val Thr Val Ser Pro Tyr Thr Glu
 225 230 235 240

Ile His Leu Lys Lys Tyr Gln Ile Phe Ser Gly Thr Ser Lys Arg Thr

	245		250		255										
Val	Leu	Leu	Thr	Gly	Met	Glu	Gly	Ile	Gln	Met	Asp	Glu	Glu	Ile	Val
	260							265				270			
Glu	Asp	Leu	Ile	Asn	Ile	His	Phe	Gln	Arg	Ala	Lys	Asn	Gly	Gly	Gly
	275						280					285			
Glu	Val	Asp	Val	Val	Lys	Cys	Ser	Leu	Gly	Gln	Pro	His	Ile	Ala	Tyr
	290					295					300				
Phe	Glu	Glu													
305															

<210> 8
 <211> 659
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(659)
 <223> for any n in the sequence, n is an undefined base

<400> 8	
agcaggtgct gcaacaaaag gagcacacga tcaacatgga ggagtgccgg ctgcgggtgc	60
agggtccagcc cttggagctg cccatggtca ccaccatcca ggtgtccagc cagttgagtg	120
gccggagggt gttggtcact ggatttcctg ccagcctcag gctgagtgag gaggagctgc	180
tggacaanct anagatcttc tttggcaaga ctaggaacgg aggtggcnat gtggacnttc	240
ggganctact gccagggant gtcattgctgg ggtttgctag ggatggagtg gctcancgtc	300
tgtgccaaat cggccatttc acagtgccac tgggtgggca gcangtccct ctgagagtct	360
ctccgtatgt gaatggggan atccagangg ctganatcag gtcncagcca nttccccgct	420
cggtactggt gctcaacatt cctgatattct tggatggccc ggagctgcat gacgtcctgg	480
anatccactt ccagaanccc acccgcgggg gcggagatgt aagacgccct gacagtcgta	540
ccccaaggac aacagggcct aacagtcttc acctcctgaa tcaaggctan gggcctcccc	600
cttctcatcc tccccacccc ccccgccaaa gggtctcaan actgggctg ggctttntg	659

<210> 9
 <211> 630
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(630)
 <223> for any n in the sequence, n is an undefined base

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<400> 9
ccaaaagtggc tgagcaggtg ctgcaacaaa aggagcacac gatcaacatg gaggagtgcc      60
ggctgcgggt gcaggtccag cccttggagc tgcccatggt caccaccatc caggtgtcca      120
gccagttgag tggccggagg gtgttgggtca ctggatttcc tgccagcctc aggctgagtg      180
aggaggagct gctggacaag ctagagatct tctttggcaa gactaggaac ggaggtggcg      240
atgtggacgt tcgggagcta ctgccaggga gtgtcatgct ggggtttgct agggatggag      300
tggtccagcg tctgtgccaa atcggccaag ttcacagtgc cactgggtgg gcancaagtc      360
cctctgagag tctctccgta tgtgaatggg gagatccaga aggctgagat caggtcgcan      420
ccagttcccc nctcggtagt gggtgctcaa cattcctgat atcttggatt ggcccggagc      480
tgcatnacgt cctgganata aacttcanaa gccaccgccg cggggcngng aggtanaagg      540
cctgacatcn ttaccccaaa ggacagcatg gncctaacag tcctcacctc cnaatcangc      600
tnnggggctn cccttctanc ntcccaactg      630

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<210> 10
<211> 631
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(631)
<223> for any n in the sequence, n is an undefined base

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<400> 10
ggatccactg ccctctgctt gcgggctctg ctctgatcac ctttgatgac cccaaagtgg      60
ctgagcaggt gctgcaacaa aaggagcaca cgatcaacat ggaggagtgc cggctgcggg      120
tgcaggtcca gcccttggag ctgcccattg tcaccaccat ccaggtgatg gtgtccagcc      180
anttgagtgg cgggaggggt ttgggtcact gatttcctgc cagcctcagg ctgantgagg      240
aggagctgct ggacaagcta tgagatcttc tttggcaana ctangaacgg angtggcgat      300
gtggacgttc gggagctact gccaggaggt gtcattgctg ggtttgctac ggatggagtg      360
gctcagcgtc tgtgccaaat cggccagttc acaagtgcc a ctgggtgggc agcaagtccc      420
tctgagagtc tctccgtatg tgantggnga gatcagaatg ctganattaa gtcgcatcca      480
attcctcgct cnggtactgg tgctcannat cctganatct tggattggcc ccngantnca      540
tganatctgg nagattcaat tncanaagtc canccnncng ngncgggaag tanangcccg      600
ananttctn ncntanggn agcanngcct g      631

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<210> 11

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<211> 138
 <212> PRT
 <213> Homo sapiens

<400> 11

His	Glu	Gly	Pro	Lys	Val	Ala	Glu	Gln	Val	Leu	Gln	Gln	Lys	Glu	His
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Thr	Ile	Asn	Met	Glu	Glu	Cys	Arg	Leu	Arg	Val	Gln	Val	Gln	Pro	Leu
		20						25					30		
Glu	Leu	Pro	Met	Val	Thr	Thr	Ile	Gln	Val	Ser	Ser	Gln	Leu	Ser	Gly
		35					40					45			
Arg	Arg	Val	Leu	Val	Thr	Gly	Phe	Pro	Ala	Ser	Leu	Arg	Leu	Ser	Glu
		50				55					60				
Glu	Glu	Leu	Leu	Asp	Lys	Leu	Glu	Ile	Phe	Phe	Gly	Lys	Thr	Arg	Asn
65				70					75						80
Gly	Gly	Gly	Asp	Val	Asp	Val	Arg	Glu	Leu	Leu	Pro	Gly	Ser	Val	Met
			85						90					95	
Leu	Gly	Phe	Ala	Arg	Asp	Gly	Val	Ala	Gln	Arg	Leu	Cys	Gln	Ile	Gly
			100					105					110		
Gln	Val	His	Ser	Ala	Thr	Gly	Trp	Ala	Ser	Ser	Pro	Ser	Glu	Ser	Leu
		115					120					125			
Ser	Val	Cys	Glu	Trp	Gly	Asp	Pro	Glu	Gly						
		130				135									

<210> 12
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 12

Met	Ser	Ala	Pro	Leu	Asp	Ala	Ala	Leu	His	Ala	Leu	Gln	Glu	Glu	Gln
1				5					10					15	
Ala	Arg	Leu	Lys	Met	Arg	Leu	Trp	Asp	Leu	Gln	Gln	Leu	Arg	Lys	Glu
		20						25					30		
Leu	Gly	Asp	Ser	Pro	Lys	Asp	Lys	Val	Pro	Phe	Ser	Val	Pro	Lys	Ile
		35					40					45			
Pro	Leu	Val	Phe	Arg	Gly	His	Thr	Gln	Gln	Asp	Pro	Glu	Val	Pro	Lys
		50				55					60				
Ser	Leu	Val	Ser	Asn	Leu	Arg	Ile	His	Cys	Pro	Leu	Leu	Ala	Gly	Ser
65				70					75					80	
Ala	Leu	Ile	Thr	Phe	Asp	Asp	Pro	Lys	Val	Ala	Glu	Gln	Val	Leu	Gln
			85					90						95	
Gln	Lys	Glu	His	Thr	Ile	Asn	Met	Glu	Glu	Cys	Arg	Leu	Arg	Val	Gln

100					105					110					
Val	Gln	Pro	Leu	Glu	Leu	Pro	Met	Val	Thr	Thr	Ile	Gln	Val	Ser	Ser
		115					120					125			
Gln	Leu	Ser	Gly	Arg	Arg	Val	Leu	Val	Thr	Gly	Phe	Pro	Ala	Ser	Leu
	130					135					140				
Arg	Leu	Ser	Glu	Glu	Glu	Leu	Leu	Asp	Lys	Leu	Glu	Ile	Phe	Phe	Gly
145					150					155					160
Lys	Thr	Arg	Asn	Gly	Gly	Gly	Asp	Val	Asp	Val	Arg	Glu	Leu	Leu	Pro
			165						170					175	
Gly	Ser	Val	Met	Leu	Gly	Phe	Ala	Arg	Asp	Gly	Val	Ala	Gln	Arg	Leu
			180					185					190		
Cys	Gln	Ile	Gly	Gln	Phe	Thr	Val	Pro	Leu	Gly	Gly	Gln	Gln	Val	Pro
	195						200					205			
Leu	Arg	Val	Ser	Pro	Tyr	Val	Asn	Gly	Glu	Ile	Gln	Lys	Ala	Glu	Ile
	210					215					220				
Arg	Ser	Gln	Pro	Val	Pro	Arg	Ser	Val	Leu	Val	Leu	Asn	Ile	Pro	Asp
225					230					235					240
Ile	Leu	Asp	Gly	Pro	Glu	Leu	His	Asp	Val	Leu	Glu	Ile	His	Phe	Gln
			245						250					255	
Lys	Pro	Thr	Arg	Gly	Gly	Gly	Gly	Arg	Gly	Pro	Asp	Ser	Arg	Thr	Pro
			260					265					270		
Arg	Thr	Ala	Gly	Pro	Ser	Ser	Leu	His	Leu						
	275						280								

<210> 13
 <211> 207
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(207)
 <223> for any Xaa in the sequence, Xaa is an undefined amino acid

<400> 13

His	Glu	Gly	Arg	Ile	His	Cys	Pro	Leu	Leu	Ala	Gly	Ser	Ala	Leu	Ile
1				5				10					15		
Thr	Phe	Asp	Asp	Pro	Lys	Val	Ala	Glu	Gln	Val	Leu	Gln	Gln	Lys	Glu
		20					25					30			
His	Thr	Ile	Asn	Met	Glu	Glu	Cys	Arg	Leu	Arg	Val	Gln	Val	Gln	Pro
	35						40				45				
Leu	Glu	Leu	Pro	Met	Val	Thr	Thr	Ile	Gln	Val	Met	Val	Ser	Ser	Xaa
50					55					60					

Leu Ser Gly Arg Arg Val Leu Val Thr Gly Phe Pro Ala Ser Leu Arg
 65 70 75 80
 Leu Xaa Glu Glu Glu Leu Leu Asp Lys Leu Asp Leu Leu Trp Gln Xaa
 85 90 95
 Xaa Glu Arg Xaa Trp Arg Cys Gly Arg Ser Gly Ala Thr Ala Arg Glu
 100 105 110
 Cys His Ala Gly Val Cys Tyr Gly Trp Ser Gly Ser Ala Ser Val Pro
 115 120 125
 Asn Arg Pro Val His Lys Cys His Trp Val Gly Ser Lys Ser Leu Glu
 130 135 140
 Ser Leu Arg Met Xaa Xaa Arg Ser Glu Cys Xaa Val Ala Ser Asn Ser
 145 150 155 160
 Ser Leu Xaa Tyr Trp Cys Ser Xaa Ser Xaa Leu Gly Leu Ala Pro Xaa
 165 170 175
 Xaa Met Xaa Ser Gly Arg Phe Asn Xaa Xaa Ser Pro Xaa Xaa Xaa Xaa
 180 185 190
 Gly Lys Xaa Xaa Pro Xaa Xaa Ser Xaa Xaa Xaa Xaa Ser Xaa Ala
 195 200 205

<210> 14
 <211> 647
 <212> PRT

<213> Homo sapiens

<400> 14

Arg Leu Arg Asn Gly His Val Gly Ile Ser Phe Val Pro Lys Glu Thr
 1 5 10 15
 Gly Glu His Leu Val His Val Lys Lys Asn Gly Gln His Val Ala Ser
 20 25 30
 Ser Pro Ile Pro Val Val Ile Ser Gln Ser Glu Ile Gly Asp Ala Ser
 35 40 45
 Arg Val Arg Val Ser Gly Gln Gly Leu His Glu Gly His Thr Phe Glu
 50 55 60
 Pro Ala Glu Phe Ile Ile Asp Thr Arg Asp Ala Gly Tyr Gly Gly Leu
 65 70 75 80
 Ser Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn Thr Glu Asp
 85 90 95
 Leu Glu Asp Gly Thr Cys Arg Val Thr Tyr Cys Pro Thr Glu Pro Gly
 100 105 110
 Asn Tyr Ile Ile Asn Ile Lys Phe Ala Asp Gln His Val Pro Gly Ser
 115 120 125

Pro Phe Ser Val Lys Val Thr Gly Glu Gly Arg Val Lys Glu Ser Ile
 130 135 140
 Thr Arg Arg Arg Arg Ala Pro Ser Val Ala Asn Val Gly Ser His Cys
 145 150 155 160
 Asp Leu Ser Leu Lys Ile Pro Glu Ile Ser Ile Gln Asp Met Thr Ala
 165 170 175
 Gln Val Thr Ser Pro Ser Gly Lys Thr His Glu Ala Glu Ile Val Glu
 180 185 190
 Gly Glu Asn His Thr Tyr Cys Ile Arg Phe Val Pro Ala Glu Met Gly
 195 200 205
 Thr His Thr Val Ser Val Lys Tyr Lys Gly Gln His Val Pro Gly Ser
 210 215 220
 Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu Gly Gly Ala His Lys
 225 230 235 240
 Val Arg Ala Gly Gly Pro Gly Leu Glu Arg Ala Glu Ala Gly Val Pro
 245 250 255
 Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly Ala Gly Gly Leu Ala
 260 265 270
 Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Ser Phe Glu Asp Arg
 275 280 285
 Lys Asp Gly Ser Cys Gly Val Ala Tyr Val Val Gln Glu Pro Gly Asp
 290 295 300
 Tyr Glu Val Ser Val Lys Phe Asn Glu Glu His Ile Pro Asp Ser Pro
 305 310 315 320
 Phe Val Val Pro Val Ala Ser Pro Ser Gly Asp Ala Arg Arg Leu Thr
 325 330 335
 Val Ser Ser Leu Gln Glu Ser Gly Leu Lys Val Asn Gln Pro Ala Ser
 340 345 350
 Phe Ala Val Ser Leu Asn Gly Ala Lys Gly Ala Ile Asp Ala Lys Val
 355 360 365
 His Ser Pro Ser Gly Ala Leu Glu Glu Cys Tyr Val Thr Glu Ile Asp
 370 375 380
 Gln Asp Lys Tyr Ala Val Arg Phe Ile Pro Arg Glu Asn Gly Val Tyr
 385 390 395 400
 Leu Ile Asp Val Lys Phe Asn Gly Thr His Ile Pro Gly Ser Pro Phe
 405 410 415
 Lys Ile Arg Val Gly Glu Pro Gly His Gly Gly Asp Pro Gly Leu Val
 420 425 430
 Ser Ala Tyr Gly Ala Gly Leu Glu Gly Gly Val Thr Gly Asn Pro Ala
 435 440 445

Glu Phe Val Val Asn Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val
 450 455 460
 Thr Ile Asp Gly Pro Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro
 465 470 475 480
 Glu Gly Tyr Arg Val Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu
 485 490 495
 Ile Ser Ile Lys Tyr Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe
 500 505 510
 Lys Ala Lys Val Thr Gly Pro Arg Leu Val Ser Asn His Ser Leu His
 515 520 525
 Glu Thr Ser Ser Val Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala
 530 535 540
 Pro Gln His Gly Ala Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val
 545 550 555 560
 Val Ala Lys Gly Leu Gly Leu Ser Lys Ala Tyr Val Gly Gln Lys Ser
 565 570 575
 Ser Phe Thr Val Asp Cys Ser Lys Ala Gly Asn Asn Met Leu Leu Val
 580 585 590
 Gly Val His Gly Pro Arg Thr Pro Cys Glu Glu Ile Leu Val Lys His
 595 600 605
 Val Gly Ser Arg Leu Tyr Ser Val Ser Tyr Leu Leu Lys Asp Lys Gly
 610 615 620
 Glu Tyr Thr Leu Val Val Lys Trp Gly His Glu His Ile Pro Gly Ser
 625 630 635 640
 Pro Tyr Arg Val Val Val Pro
 645

<210> 15
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 15

His Glu Gly Arg Gly Val Thr Gly Asn Pro Ala Glu Phe Val Val Asn
 1 5 10 15
 Thr Ser Asn Ala Gly Ala Gly Ala Leu Ser Val Thr Ile Asp Gly Pro
 20 25 30
 Ser Lys Val Lys Met Asp Cys Gln Glu Cys Pro Glu Gly Tyr Arg Val
 35 40 45
 Thr Tyr Thr Pro Met Ala Pro Gly Ser Tyr Leu Ile Ser Ile Lys Tyr
 50 55 60

Gly Gly Pro Tyr His Ile Gly Gly Ser Pro Phe Lys Ala Lys Val Thr
 65 70 75 80
 Gly Pro Arg Leu Val Ser Asn His Ser Leu His Glu Thr Ser Ser Val
 85 90 95
 Phe Val Asp Ser Leu Thr Lys Ala Thr Cys Ala Pro His His Gly Ala
 100 105 110
 Pro Gly Pro Gly Pro Ala Asp Ala Ser Lys Val Val Ala Lys Gly Leu
 115 120 125
 Gly Leu Ser Lys Ala Tyr Val Cys His Lys Ser Ser Phe Thr Val Asp
 130 135 140
 Cys Ser Lys Ala Cys Ile Ile Met Leu Leu Val Gly Val His Gly Pro
 145 150 155 160
 Trp Thr Pro Cys Asp Glu Ile Leu Val Lys Ala Arg Gly Gln Pro Ala
 165 170 175
 Leu Gln Arg Val Leu Thr Cys Phe Lys Asp Lys Gly Glu Val His Thr
 180 185 190
 Gly Gly Gln Asn Gly Gly Asp Tyr Gln Ile Pro Cys Lys Pro Leu Pro
 195 200 205
 Leu Cys Gly Cys Pro
 210

<210> 16
 <211> 213
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)...(213)
 <223> for any Xaa in the sequence, Xaa is an undefined amino acid

 <400> 16

His Glu Gly Arg Pro Thr Glu Pro Gly Asn Tyr Ile Ile Asn Ile Lys
 1 5 10 15
 Phe Ala Asp Gln His Val Pro Gly Ser Pro Phe Ser Val Lys Val Thr
 20 25 30
 Gly Glu Gly Arg Val Lys Glu Ser Ile Thr Arg Arg Arg Arg Ala Pro
 35 40 45
 Ser Val Ala Asn Val Gly Ser His Cys Asp Leu Ser Leu Lys Ile Pro
 50 55 60
 Glu Ile Ser Ile Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly
 65 70 75 80
 Lys Thr His Glu Ala Glu Ile Val Glu Gly Glu Asn His Thr Tyr Cys
 85 90 95

Ile Arg Phe Val Pro Ala Glu Met Gly Thr His Thr Val Ser Val Lys
 100 105 110
 Tyr Lys Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly
 115 120 125
 Pro Leu Gly Glu Gly Gly Ala His Xaa Val Arg Ala Gly Gly Pro Gly
 130 135 140
 Leu Xaa Lys Ser Ser Trp Ser Ala Ser Arg Ile Gln Tyr Leu Gly Pro
 145 150 155 160
 Gly Lys Leu Val Leu Glu Ala Trp Pro Leu Leu Ser Xaa Ala Pro Ala
 165 170 175
 Xaa Leu Xaa Ser Leu Leu Arg Thr Ala Arg Thr Ala Pro Val Val Leu
 180 185 190
 Leu Met Leu Val Xaa Glu Pro Ser Asp Xaa Asn Pro Xaa Gln Val Ser
 195 200 205
 Thr Lys Glu His Xaa
 210

<210> 17
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <223> Myc-tag peptide

<400> 17

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10